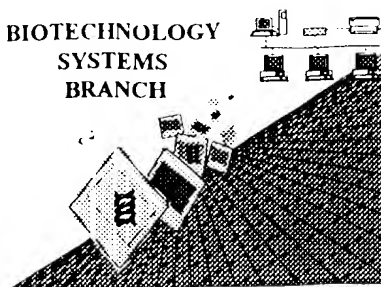


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/727,855A

Source: 1645

Date Processed by STIC: 6/7/2001

RECEIVED

JUN 27 2001

TECH CENTER 1600/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

JUN 27 1998

Raw Sequence Listing Error Summary

TECH CENTER 1001 2001

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER: 09/722,855A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 1 Wrapped Aminos
- 2 Invalid Line Length The rules require that a line **not** exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 3 Numbering
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your **subsequent submission is saved in ASCII text**.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 6 "bug"
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 7 (OLD RULES)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 8 (NEW RULES)
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1645

RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

f.b

3 <110> APPLICANT: F. HOFFMANN-LA ROCHE AG
 5 <120> TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND
 6 BIOLOGICALLY USEFUL MATERIALS THEREOF
 8 <130> FILE REFERENCE: SOD

C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/727,855A
 C--> 11 <141> CURRENT FILING DATE: 2000-12-01

13 <150> PRIOR APPLICATION NUMBER: EP99123821.3
 14 <151> PRIOR FILING DATE: 1999-12-01
 16 <160> NUMBER OF SEQ ID NOS: 17
 18 <170> SOFTWARE: PatentIn Ver. 2.0
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 21 <211> LENGTH: 3632
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Phaffia rhodozyma
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RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

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88 <222> LOCATION: (2391)..(2507)
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91 <221> NAME/KEY: polyA_site
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100 agtatgacga tggtagaggt gaaggaggga accacaggtt gaccagtctc aaagagtgtc 180
102 gatgtgcgcg aggattttgtc attaaatggt gttgtatatg cttagagcaa gagaagacat 240
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106 ctcaactaac caagaagcca ggatcaggag gaatgcctcc cctttttcat caagatcttt 360
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110 ccattgtatc gactttgtct gacttgcctt tcttatctct gacgagagat gggcattcca 480
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120 cgaacgaaaa gaacagaaga gctggtaagt cagtcagtcg gtcagtcagt caatcaaaaa 780
122 ctggtgtcta gggttataga tcgacgcgac gcgacgcgtt tgagacgca tatgcttacg 840
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126 ttcaaaaaggc tttctccatc ttaagctcat tctcatctaa ccgactcctc tcgttcccat 960
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140 gaaaattcct ctcaactcag gcc ctg gag ccc tcc atc tcc aag gag atc atg 1339
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144 gct gcc gag gag agc tac teg gcc gct gtg ggc aag gag gat gtg ctt 1435
146 acc cag gtt aag ctt cag tct gtaagctga cgttttttt atcgaccgga 1486
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RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

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Output Set: C:\CRF3\06072001\I727855A.raw

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156 tgg aag aac ttg gct ccc tat gga tcc gag gag gct acc ctg tct gaa 1753
158 gga cct ctg aag aag gct atc gag gaa tct ttt ggt tct ttc gag g 1799
160 gtcgtccat ctattcttct attcagttgt gtttggttcc ggtatactca tctgtttgt 1859
162 tttcccaaaa aataaaaaata aaaattttgt cctctcggg ggttcgactg caagttcata 1919
164 g cc ttc aag aag aag ttc aac gct gac acc gct gct gtc caa gga tcc 1967
166 gga tgg ggc tgg ctt gtatgtatca tatectttcc atctcaaaact cttctcagag 2022
168 tttttttct tgagacttca aactgactat acatgtttct acaacaaaaca acag ggc 2079
170 ttg aac ccg ctt act aag aag ctg gaa gtc acc acg acc gcc aac cag 2127
172 gac cct ctg ctt a gtaagttgt tctacatgat tttctatctc aacggatct 2180
174 gcattgattcg tcaactgattc actggattct cttgtttcgt tttctcggg atgatttcat 2240
176 aaacag ct cac att cct atc atc gga gtt gac gtgcgtatct ttctgaata 2292
178 gtgtagcgt ctgattctgt tttattgact gacgtgttg tctgtccaa atcattaaaa 2352
180 aaatatgaaa caataatcg attgacggac gaaaacag atc tgg gag cac gct ttc 2408
182 tac ctt cag tac aag aac gtc aag cct gac tat ctg gct gct gtt tgg 2456
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188 cataaacaac tttogaggca gatgggagag tacgtacaag agaggtttgt atggagaatt 2617
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192 agaagagaac aagatggttt gtccgaagag attgagagat caagcccggt catctgagt 2737
194 cgaacaaaaca tgccttggtc tgcacacagt ttctagcaca ttatgaacct gttcatgtgt 2797
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206 ggcgctctgc tgttcgggaa aagaaaaggc aaaaagggaac agagcgataa gcatatgtga 3157
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210 gacgttctca agctgctgct tggaaagctt tccgagcttg ccagtaggtc cctggttgga 3277
212 gaagaagatg togaaggcta agggcgatga aaagcatgaa gatattagct atcggcgoga 3337
214 taaaagtgtg acgagatgaa aatggagaaa agatgattcg caccatcgac gacctogacc 3397
216 aaagggaatg aggtgtcacc ggcttccac ttctgtact cctcaacggt gacgaagatg 3457
218 acgaagcagt cgttggcctt agctcgggc tcttagatgc tgatgaaaca caataggtag 3517
220 taggagagga gaaagagaag atgatgatg gtcaggatgc ttgttccact gtagatggag 3577
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225 <210> SEQ ID NO: 2

226 <211> LENGTH: 3375

227 <212> TYPE: DNA

228 <213> ORGANISM: Phaffia rhodozyma

230 <220> FEATURE:

231 <221> NAME/KEY: 5'UTR

232 <222> LOCATION: (974)..(975)

233 <223> OTHER INFORMATION: EXPERIMENTAL

235 <230> FEATURE:

236 <231> NAME/KEY: exon

237 <232> LOCATION: (1040)..(1063)

239 <240> FEATURE:

240 <241> NAME/KEY: intron

RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

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301 <222> LOCATION: (2239)..(2293)
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305 <222> LOCATION: (2294)..(2376)

RAW SEQUENCE LISTING

DATE: 06/07/2001

PATENT APPLICATION: US/09/727,855A

TIME: 14:25:41

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

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311 <220> FEATURE:
312 <221> NAME/KEY: intron
313 <222> LOCATION: (2427)..(2524)
315 <220> FEATURE:
316 <221> NAME/KEY: exon
317 <222> LOCATION: (2525)..(2542)
319 <220> FEATURE:
320 <221> NAME/KEY: polyA_site
321 <222> LOCATION: (2667)..(2668)
322 <223> OTHER INFORMATION: EXPERIMENTAL
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329 tgttgacaga tgaaaggacg aactatgaag ctgtccatgc tccccaaacc gattgacaca 180
331 cgcgcgtcag gcaacgcaga atttctcact gcttcgacgt cacaccaaca tcgatcctcc 240
333 atacctaaaa gcagatcgag acacattggt ggtcgccatg ttggatggat gtacatcaaa 300
335 cccacagcat atatcactca catgtgagaa ctccgtagcc tctaccttct tgtctctcaa 360
337 tctgaatgtc tggttgagag gtggaatgaa tgtttacagt ttgagaagac gaaagaaaga 420
339 aagagaagag aagagaggaa tacgtacgac gaagttatca tcgtatggga actttttctaa 480
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343 cgagcaagtc tgggcaagtg catccttcgt ctacaagaaa gagaccagga aatgaaggag 600
345 agaagagtaa gcaggtacct accgatattg gatcgttctc tctaccagc gatgccttca 660
347 ccaagcgttc tatctcttct tgggatggca gatacatact taacgagagc aatctgatgt 720
349 ataccgaact tgaacggaa tgatcccaga atcctcttga acccttgaac ccttgaacct 780
351 tggaaccaag taaccaaccg gcaaacgcgc gatacggctc acaccacaga accacacgcc 840
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369 gttgttccgg ttgcacacga tagctaactg tctctcgttc ctcaatatga acatgcag 1358
371 aa atc atg atc ctt cac cac tcc aag cac cat cag act tac gtc 1402
373 gtaagtaate taaaggtcat ctccgtctac atggccggat caacttctc atagatcttc 1462
375 cttctgttgc ggcctacgta g acc aac ctg aac gcc gct atc cag gct ttc 1513
377 tcc cag acc aat gac atc aag gcc cag atc gct ctt cag agc gct ctg 1561
379 aag ttc aac gga gga gga cac atc aac c gtacgatcat tctcctctt 1609
381 ctggtttatc atatgtgttg cttgtcacta acacgcagtc aaccccgga tatctcacc 1669
383 tgtag ac tcc ctg ttc tgg aag aac atg gct cct gcc gac tct gct gat 1718
385 gcc aag ctg acc gag gga tgg ctg aag act gcc atc gac aag gac ttt 1766
387 gga tcc ttc gag gag ttc aag aag aag ttc aac act gct act ctg ggt 1814
389 gtc cag gga tct gtcagtatct cgtttgcttc gacatactct cagctttcct 1866
391 tccgtaaaact gacgaatagt ttttcggaca tgtacttgta g gga tgg gga tgg ctg 1922
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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Sod1(sense
 primer for cloning of SOD genes)

<400> 10
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→ see item 9 on Encl Summary Sheet

23

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Sod4 (antisense
 primer for cloning of SOD genes)

<400> 11
 gccacacng anccytgnac ncc

↓
 item 9

23

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/727,855A

DATE: 06/07/2001

TIME: 14:25:42

Input Set : A:\SeqListing.txt

Output Set: C:\CRF3\06072001\I727855A.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:881 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:881 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:894 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:894 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:963 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:963 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:976 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:976 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17